



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 08:22 AM BST

PDB ID : 2PGZ  
Title : Crystal structure of Cocaine bound to an ACh-Binding Protein  
Authors : Hansen, S.B.; Taylor, P.  
Deposited on : 2007-04-10  
Resolution : 1.76 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

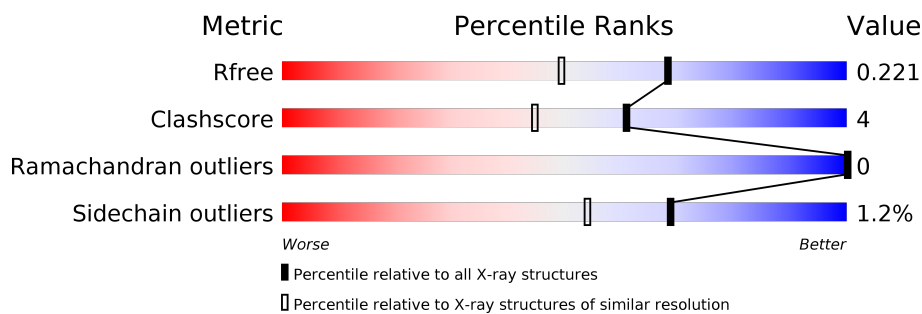
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	230	87% 5% 8%
1	B	230	83% 8% 8%
1	C	230	82% 9% 8%
1	D	230	86% 7% 7%
1	E	230	81% 10% 9%
2	F	5	20% 80%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9900 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	6	0
			1721	1085	285	343	8			
1	B	211	Total	C	N	O	S	0	2	0
			1695	1072	276	339	8			
1	C	211	Total	C	N	O	S	0	7	0
			1728	1091	286	341	10			
1	D	214	Total	C	N	O	S	0	5	0
			1742	1100	285	348	9			
1	E	209	Total	C	N	O	S	0	9	0
			1718	1086	282	341	9			

There are 55 discrepancies between the modelled and reference sequences:

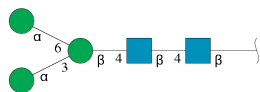
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	cloning artifact	UNP Q8WSF8
A	-7	TYR	-	cloning artifact	UNP Q8WSF8
A	-6	LYS	-	cloning artifact	UNP Q8WSF8
A	-5	ASP	-	cloning artifact	UNP Q8WSF8
A	-4	ASP	-	cloning artifact	UNP Q8WSF8
A	-3	ASP	-	cloning artifact	UNP Q8WSF8
A	-2	ASP	-	cloning artifact	UNP Q8WSF8
A	-1	LYS	-	cloning artifact	UNP Q8WSF8
A	0	LEU	-	cloning artifact	UNP Q8WSF8
A	220	SER	-	cloning artifact	UNP Q8WSF8
A	221	ARG	-	cloning artifact	UNP Q8WSF8
B	-8	ASP	-	cloning artifact	UNP Q8WSF8
B	-7	TYR	-	cloning artifact	UNP Q8WSF8
B	-6	LYS	-	cloning artifact	UNP Q8WSF8
B	-5	ASP	-	cloning artifact	UNP Q8WSF8
B	-4	ASP	-	cloning artifact	UNP Q8WSF8
B	-3	ASP	-	cloning artifact	UNP Q8WSF8
B	-2	ASP	-	cloning artifact	UNP Q8WSF8
B	-1	LYS	-	cloning artifact	UNP Q8WSF8

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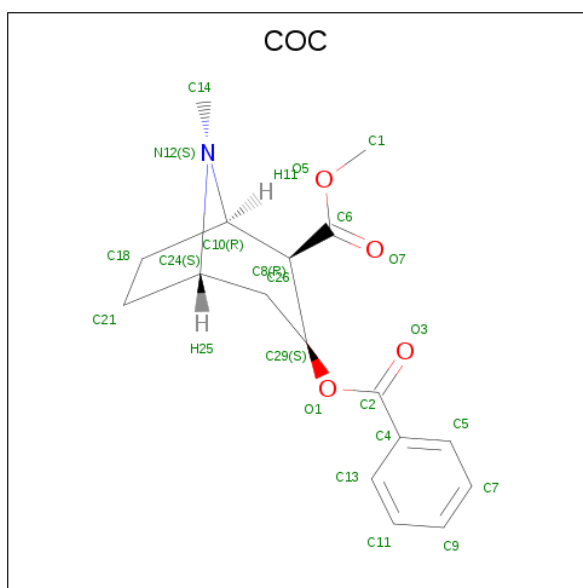
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	LEU	-	cloning artifact	UNP Q8WSF8
B	220	SER	-	cloning artifact	UNP Q8WSF8
B	221	ARG	-	cloning artifact	UNP Q8WSF8
C	-8	ASP	-	cloning artifact	UNP Q8WSF8
C	-7	TYR	-	cloning artifact	UNP Q8WSF8
C	-6	LYS	-	cloning artifact	UNP Q8WSF8
C	-5	ASP	-	cloning artifact	UNP Q8WSF8
C	-4	ASP	-	cloning artifact	UNP Q8WSF8
C	-3	ASP	-	cloning artifact	UNP Q8WSF8
C	-2	ASP	-	cloning artifact	UNP Q8WSF8
C	-1	LYS	-	cloning artifact	UNP Q8WSF8
C	0	LEU	-	cloning artifact	UNP Q8WSF8
C	220	SER	-	cloning artifact	UNP Q8WSF8
C	221	ARG	-	cloning artifact	UNP Q8WSF8
D	-8	ASP	-	cloning artifact	UNP Q8WSF8
D	-7	TYR	-	cloning artifact	UNP Q8WSF8
D	-6	LYS	-	cloning artifact	UNP Q8WSF8
D	-5	ASP	-	cloning artifact	UNP Q8WSF8
D	-4	ASP	-	cloning artifact	UNP Q8WSF8
D	-3	ASP	-	cloning artifact	UNP Q8WSF8
D	-2	ASP	-	cloning artifact	UNP Q8WSF8
D	-1	LYS	-	cloning artifact	UNP Q8WSF8
D	0	LEU	-	cloning artifact	UNP Q8WSF8
D	220	SER	-	cloning artifact	UNP Q8WSF8
D	221	ARG	-	cloning artifact	UNP Q8WSF8
E	-8	ASP	-	cloning artifact	UNP Q8WSF8
E	-7	TYR	-	cloning artifact	UNP Q8WSF8
E	-6	LYS	-	cloning artifact	UNP Q8WSF8
E	-5	ASP	-	cloning artifact	UNP Q8WSF8
E	-4	ASP	-	cloning artifact	UNP Q8WSF8
E	-3	ASP	-	cloning artifact	UNP Q8WSF8
E	-2	ASP	-	cloning artifact	UNP Q8WSF8
E	-1	LYS	-	cloning artifact	UNP Q8WSF8
E	0	LEU	-	cloning artifact	UNP Q8WSF8
E	220	SER	-	cloning artifact	UNP Q8WSF8
E	221	ARG	-	cloning artifact	UNP Q8WSF8

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is COCAINE (three-letter code: COC) (formula:  $C_{17}H_{21}NO_4$ ).



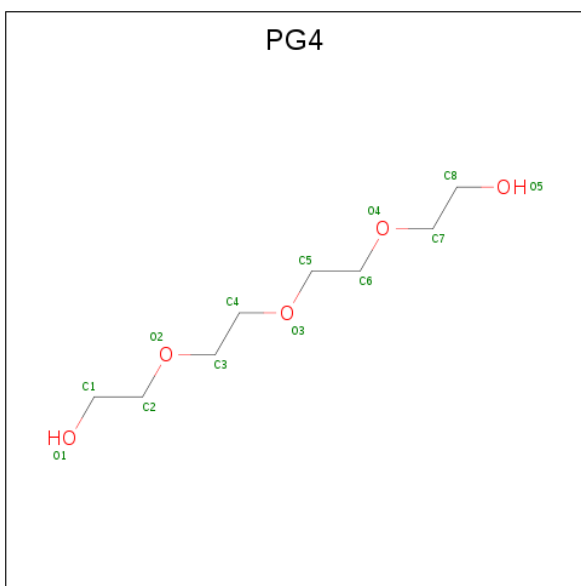
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 22	C 17	N 1	O 4	0	0
3	D	1	Total 22	C 17	N 1	O 4	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $\text{C}_8\text{H}_{15}\text{NO}_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula:  $C_8H_{18}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	8	5		
5	C	1	Total	C	O	0	0
			10	6	4		
5	E	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	251	Total 251	O 251	0	6
6	B	229	Total 229	O 229	0	2
6	C	230	Total 230	O 230	0	8
6	D	223	Total 223	O 223	0	2
6	E	208	Total 208	O 208	0	6

### 3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

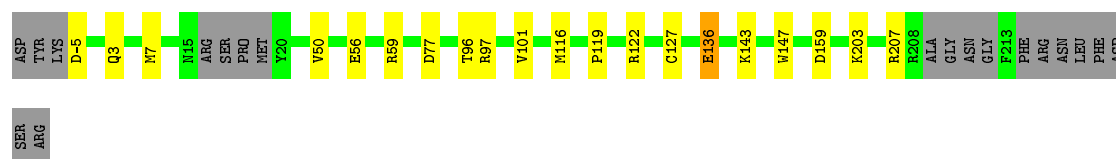
- Molecule 1: Soluble acetylcholine receptor

Chain A: 




- Molecule 1: Soluble acetylcholine receptor

Chain B: 




- Molecule 1: Soluble acetylcholine receptor

Chain C: 




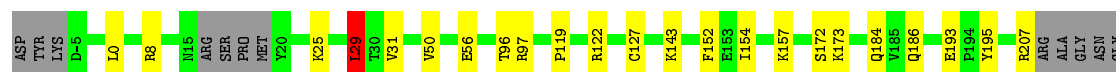
- Molecule 1: Soluble acetylcholine receptor

Chain D: 



- Molecule 1: Soluble acetylcholine receptor

Chain E: 





PHE  
PHE  
ARG  
ASN  
LEU  
PHE  
ASP  
SER  
ARG

- Molecule 2:  $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-6)] $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose

Chain F:  20% 80%

MAN1  
MAN2  
MAN3  
MAN4  
MAN5

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.82Å 115.59Å 130.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.76 47.62 – 1.76	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-1.76) 99.5 (47.62-1.76)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.180 , 0.210 0.191 , 0.221	Depositor DCC
$R_{free}$ test set	1314 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 36.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9900	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, COC, BMA, NAG, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.53	0/1777	0.61	0/2418
1	B	0.54	0/1740	0.63	0/2369
1	C	0.49	0/1787	0.64	0/2428
1	D	0.61	1/1796 (0.1%)	0.66	0/2443
1	E	0.65	3/1787 (0.2%)	0.76	3/2430 (0.1%)
All	All	0.57	4/8887 (0.0%)	0.66	3/12088 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	8	ARG	NE-CZ	11.91	1.48	1.33
1	E	8	ARG	CG-CD	8.34	1.72	1.51
1	D	-8	ASP	N-CA	6.38	1.59	1.46
1	E	8	ARG	CZ-NH2	5.43	1.40	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	8	ARG	NE-CZ-NH1	-16.74	111.93	120.30
1	E	8	ARG	NE-CZ-NH2	10.15	125.37	120.30
1	E	29	LEU	CA-CB-CG	5.31	127.52	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1721	0	1659	9	0
1	B	1695	0	1615	19	0
1	C	1728	0	1675	21	0
1	D	1742	0	1675	15	1
1	E	1718	0	1661	16	1
2	F	61	0	52	0	0
3	A	22	0	21	1	0
3	D	22	0	21	0	0
4	B	14	0	13	0	0
5	B	13	0	18	3	0
5	C	10	0	13	0	0
5	E	13	0	18	2	0
6	A	251	0	0	3	0
6	B	229	0	0	8	0
6	C	230	0	0	7	0
6	D	223	0	0	2	0
6	E	208	0	0	5	0
All	All	9900	0	8441	77	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (77) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:97[B]:ARG:HG3	6:C:633[B]:HOH:O	1.45	1.12
1:A:97[B]:ARG:NE	6:A:650[B]:HOH:O	1.65	1.00
5:B:403:PG4:H62	6:B:611:HOH:O	1.78	0.83
1:A:97[B]:ARG:CZ	6:A:650[B]:HOH:O	2.16	0.79
1:C:207[A]:ARG:HD3	6:C:635[A]:HOH:O	1.82	0.78
1:C:207[A]:ARG:HH11	1:C:207[A]:ARG:CG	1.97	0.78
1:C:207[A]:ARG:HH11	1:C:207[A]:ARG:HG2	1.49	0.78
1:A:97[B]:ARG:NH2	6:A:650[B]:HOH:O	2.17	0.75
1:C:59[B]:ARG:NH1	1:C:159:ASP:OD2	2.17	0.75
1:D:105:GLN:OE1	6:D:580:HOH:O	2.04	0.74
1:B:101:VAL:HG13	6:B:632:HOH:O	1.87	0.73
1:B:59:ARG:NH1	1:B:159:ASP:OD2	2.21	0.73
1:A:59[A]:ARG:NH1	1:A:159:ASP:OD2	2.23	0.71
1:C:191:CYS:HB3	1:C:193:GLU:OE2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:GLN:OE1	6:D:594:HOH:O	2.12	0.67
5:E:403:PG4:H32	6:E:587:HOH:O	1.95	0.67
1:B:147:TRP:O	5:B:403:PG4:H82	1.95	0.66
1:D:185:VAL:HG13	1:D:196:ILE:CD1	2.27	0.65
1:A:11:SER:HA	1:A:15:ASN:HD22	1.62	0.63
1:E:29:LEU:HD21	1:E:31:VAL:HG23	1.80	0.63
1:D:97[A]:ARG:HH21	1:D:124:SER:CB	2.13	0.62
1:C:203[B]:LYS:HG3	6:C:565:HOH:O	1.99	0.61
1:C:21:PRO:HB3	1:D:7:MET:CE	2.31	0.60
1:D:143:LYS:HZ2	1:D:184:GLN:HE22	1.50	0.60
5:E:403:PG4:H21	6:E:587:HOH:O	2.01	0.59
1:D:143:LYS:NZ	1:D:184:GLN:HE22	2.00	0.59
1:E:29:LEU:HD21	1:E:31:VAL:CG2	2.34	0.57
1:B:203[B]:LYS:HG3	6:B:623:HOH:O	2.05	0.57
1:D:7:MET:CE	1:D:7:MET:HA	2.34	0.57
1:E:143[A]:LYS:HE2	1:E:184:GLN:HE22	1.70	0.56
1:C:97[B]:ARG:CG	6:C:633[B]:HOH:O	2.24	0.56
1:C:161[A]:ASP:HB3	6:C:624:HOH:O	2.05	0.56
1:B:59:ARG:HG2	1:B:116:MET:HG3	1.88	0.56
1:B:96:THR:O	1:C:122:ARG:HD2	2.06	0.56
1:C:7:MET:HG2	6:C:505:HOH:O	2.06	0.55
1:C:207[A]:ARG:CG	1:C:207[A]:ARG:NH1	2.66	0.55
1:C:97[A]:ARG:NH1	6:C:442:HOH:O	2.39	0.54
1:B:136:GLU:CD	1:B:136:GLU:H	2.12	0.53
1:D:7:MET:HA	1:D:7:MET:HE2	1.90	0.52
1:B:59:ARG:CG	1:B:116:MET:HG3	2.40	0.52
1:C:96:THR:O	1:D:122:ARG:HD2	2.10	0.52
1:E:29:LEU:CD2	1:E:31:VAL:HG23	2.39	0.52
1:D:50:VAL:HG21	1:D:127:CYS:SG	2.50	0.51
1:A:96:THR:O	1:B:122:ARG:HD2	2.11	0.51
1:B:59:ARG:HD3	1:B:116:MET:HE2	1.93	0.50
1:A:122:ARG:HD2	1:E:96:THR:O	2.12	0.50
1:B:3:GLN:O	1:B:7:MET:HG3	2.11	0.50
1:E:157:LYS:NZ	6:E:562:HOH:O	2.43	0.50
1:C:50:VAL:HG21	1:C:127:CYS:SG	2.52	0.49
1:D:96:THR:O	1:E:122:ARG:HD2	2.13	0.49
1:B:59:ARG:HD3	1:B:116:MET:CE	2.43	0.48
1:B:97[B]:ARG:HD3	6:B:476:HOH:O	2.13	0.48
1:B:143:LYS:NZ	6:B:532:HOH:O	2.45	0.48
1:E:25:LYS:HE2	1:E:152:PHE:CD2	2.48	0.48
1:B:50:VAL:HG21	1:B:127:CYS:SG	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:TYR:CG	3:A:401:COC:H15	2.50	0.47
1:E:25:LYS:HG3	1:E:152:PHE:HB3	1.96	0.46
1:C:61:LYS:HE3	1:C:112:ASP:O	2.15	0.46
1:E:50:VAL:HG21	1:E:127:CYS:SG	2.56	0.46
1:E:29:LEU:HD22	1:E:154:ILE:HG12	1.97	0.45
1:C:21:PRO:HB3	1:D:7:MET:HE1	1.97	0.45
1:E:97[A]:ARG:HD2	6:E:609[A]:HOH:O	2.17	0.45
1:B:56:GLU:O	1:B:119:PRO:HD2	2.16	0.44
5:B:403:PG4:H12	6:B:611:HOH:O	2.18	0.44
1:E:172:SER:O	1:E:207[A]:ARG:NH2	2.50	0.44
1:E:97[A]:ARG:HD3	6:E:476:HOH:O	2.17	0.44
1:B:3:GLN:HB3	1:B:7:MET:HE3	1.99	0.44
1:A:50:VAL:HG21	1:A:127:CYS:SG	2.59	0.43
1:D:185:VAL:HG13	1:D:196:ILE:HD13	2.01	0.42
1:C:14:PHE:C	1:C:16:ARG:H	2.23	0.42
1:B:7:MET:HG2	6:B:597:HOH:O	2.19	0.41
1:E:193:GLU:HG2	1:E:195:TYR:CE2	2.55	0.41
1:E:56:GLU:O	1:E:119:PRO:HD2	2.21	0.41
1:B:207:ARG:HD3	6:B:523:HOH:O	2.20	0.40
1:C:172:SER:N	1:C:207[B]:ARG:HH11	2.18	0.40
1:C:56:GLU:O	1:C:119:PRO:HD2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:-7:TYR:OH	1:E:173:LYS:O[2_554]	2.12	0.08

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	212/230 (92%)	210 (99%)	2 (1%)	0	100	100
1	B	208/230 (90%)	206 (99%)	2 (1%)	0	100	100
1	C	213/230 (93%)	208 (98%)	5 (2%)	0	100	100
1	D	214/230 (93%)	212 (99%)	2 (1%)	0	100	100
1	E	213/230 (93%)	210 (99%)	3 (1%)	0	100	100
All	All	1060/1150 (92%)	1046 (99%)	14 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	198/208 (95%)	196 (99%)	2 (1%)	76	63
1	B	193/208 (93%)	190 (98%)	3 (2%)	62	45
1	C	199/208 (96%)	194 (98%)	5 (2%)	47	25
1	D	200/208 (96%)	199 (100%)	1 (0%)	88	83
1	E	199/208 (96%)	196 (98%)	3 (2%)	65	49
All	All	989/1040 (95%)	975 (99%)	14 (1%)	69	52

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-3	ASP
1	A	157	LYS
1	B	-5	ASP
1	B	77	ASP
1	B	136	GLU
1	C	59[A]	ARG
1	C	59[B]	ARG
1	C	186	GLN
1	C	207[A]	ARG
1	C	207[B]	ARG

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Mol	Chain	Res	Type
1	D	15	ASN
1	E	0	LEU
1	E	29	LEU
1	E	186	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	63	ASN
1	B	3	GLN
1	B	184	GLN
1	C	184	GLN
1	C	186	GLN
1	D	3	GLN
1	D	15	ASN
1	D	74	ASN
1	D	184	GLN
1	E	3	GLN
1	E	15	ASN
1	E	184	GLN
1	E	186	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

5 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the



expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	F	1	1,2	14,14,15	0.45	0	17,19,21	1.25	1 (5%)
2	NAG	F	2	2	14,14,15	0.33	0	17,19,21	1.03	1 (5%)
2	BMA	F	3	2	11,11,12	0.40	0	15,15,17	0.69	0
2	MAN	F	4	2	11,11,12	0.47	0	15,15,17	1.22	1 (6%)
2	MAN	F	5	2	11,11,12	0.53	0	15,15,17	0.99	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1
2	MAN	F	4	2	-	0/2/19/22	0/1/1/1
2	MAN	F	5	2	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	4	MAN	C1-O5-C5	3.99	117.60	112.19
2	F	1	NAG	C2-N2-C7	3.99	128.58	122.90
2	F	2	NAG	C1-C2-N2	-3.20	105.02	110.49
2	F	5	MAN	C1-O5-C5	2.41	115.46	112.19
2	F	5	MAN	C1-C2-C3	2.38	112.59	109.67

There are no chirality outliers.

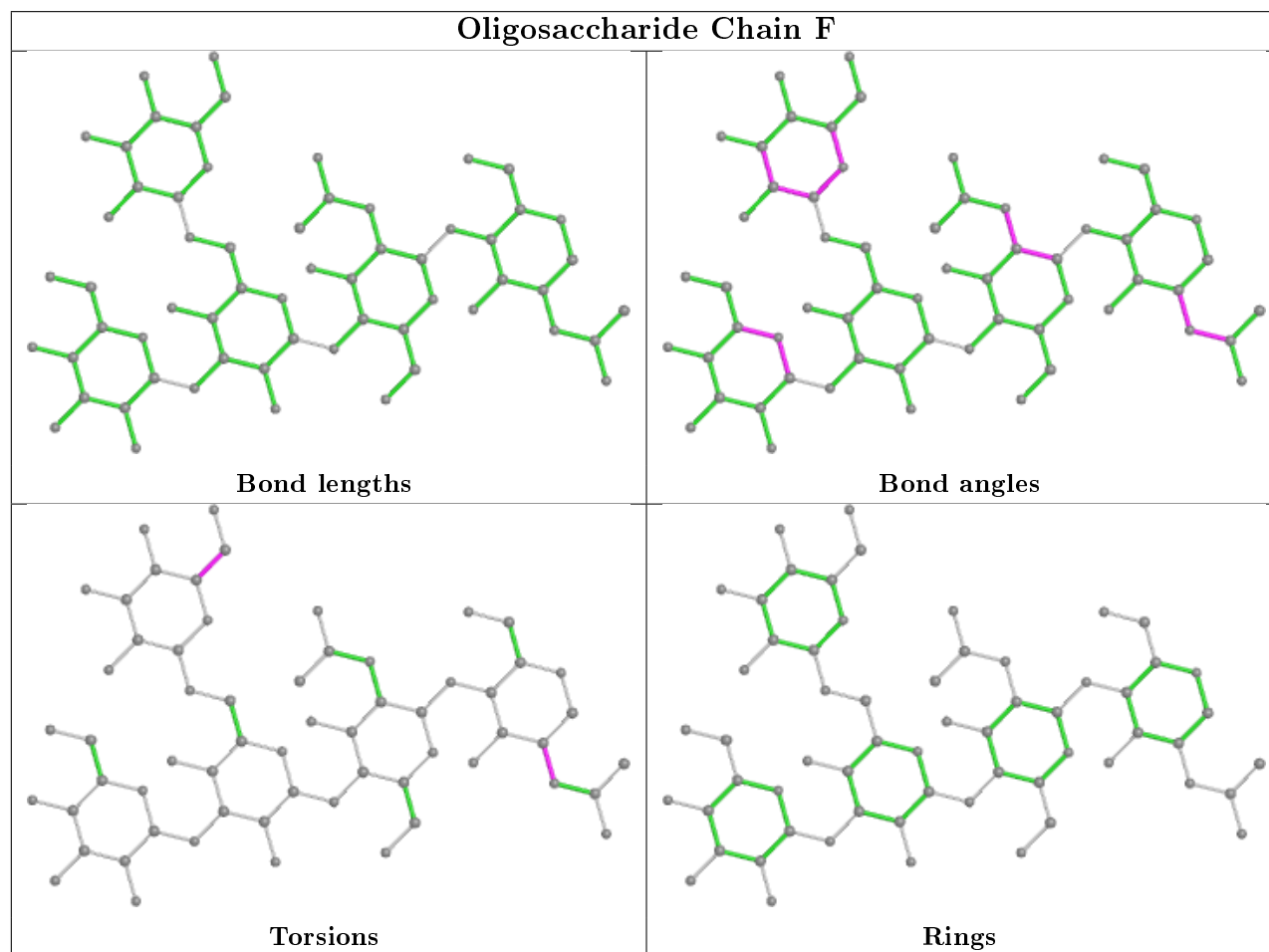
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1	NAG	C1-C2-N2-C7
2	F	5	MAN	C4-C5-C6-O6
2	F	1	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	B	402	1	14,14,15	3.39	4 (28%)	17,19,21	3.04	5 (29%)
5	PG4	C	407	-	9,9,12	1.18	1 (11%)	8,8,11	0.82	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PG4	E	403	-	12,12,12	0.52	0	11,11,11	0.27	0
3	COC	D	401	-	24,24,24	1.76	3 (12%)	32,34,34	2.55	12 (37%)
3	COC	A	401	-	24,24,24	1.62	3 (12%)	32,34,34	2.95	8 (25%)
5	PG4	B	403	-	12,12,12	1.54	3 (25%)	11,11,11	0.64	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	402	1	-	2/6/23/26	0/1/1/1
5	PG4	C	407	-	-	3/7/7/10	-
5	PG4	E	403	-	-	8/10/10/10	-
3	COC	D	401	-	-	1/14/39/39	0/4/3/3
3	COC	A	401	-	-	0/14/39/39	0/4/3/3
5	PG4	B	403	-	-	7/10/10/10	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	NAG	C7-N2	8.95	1.65	1.34
4	B	402	NAG	O7-C7	7.06	1.39	1.23
3	D	401	COC	O5-C6	5.40	1.46	1.33
3	D	401	COC	O1-C2	5.31	1.45	1.34
3	A	401	COC	O1-C2	4.60	1.44	1.34
3	A	401	COC	O5-C6	4.37	1.43	1.33
4	B	402	NAG	O6-C6	4.31	1.60	1.42
5	B	403	PG4	O3-C5	3.32	1.56	1.42
3	A	401	COC	O1-C29	-3.08	1.40	1.46
3	D	401	COC	O1-C29	-2.30	1.42	1.46
5	C	407	PG4	O3-C4	2.23	1.51	1.42
4	B	402	NAG	C8-C7	2.18	1.55	1.50
5	B	403	PG4	C4-C3	2.11	1.59	1.49
5	B	403	PG4	O2-C3	2.06	1.51	1.42

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	COC	C18-C10-N12	-12.54	92.26	105.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	NAG	C2-N2-C7	-9.43	109.47	122.90
3	D	401	COC	C18-C10-N12	-8.16	96.77	105.18
4	B	402	NAG	C8-C7-N2	-6.42	105.23	116.10
3	D	401	COC	O5-C6-C8	5.73	119.38	111.03
3	A	401	COC	C21-C24-N12	-5.42	93.77	104.44
3	A	401	COC	O5-C6-C8	4.75	117.95	111.03
3	D	401	COC	C14-N12-C24	4.09	123.06	113.25
3	D	401	COC	C14-N12-C10	3.76	122.60	113.46
3	D	401	COC	O1-C2-C4	3.59	117.72	111.92
4	B	402	NAG	C1-C2-N2	-3.54	104.43	110.49
3	A	401	COC	C14-N12-C10	3.50	121.97	113.46
3	D	401	COC	C21-C24-N12	-3.43	97.67	104.44
3	A	401	COC	C14-N12-C24	3.37	121.33	113.25
3	D	401	COC	C1-O5-C6	2.97	122.66	115.94
3	A	401	COC	O5-C6-O7	-2.93	118.11	123.84
3	A	401	COC	O1-C2-C4	2.53	116.00	111.92
3	D	401	COC	O5-C6-O7	-2.52	118.91	123.84
3	D	401	COC	C21-C18-C10	2.46	107.83	104.00
3	D	401	COC	C29-O1-C2	-2.44	113.14	117.38
3	A	401	COC	C21-C18-C10	2.30	107.59	104.00
4	B	402	NAG	O6-C6-C5	-2.26	103.53	111.29
3	D	401	COC	O1-C2-O3	-2.23	119.89	123.53
3	D	401	COC	C26-C29-C8	2.14	116.17	111.93
4	B	402	NAG	C1-O5-C5	2.07	115.00	112.19

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	407	PG4	O4-C7-C8-O5
4	B	402	NAG	O7-C7-N2-C2
5	E	403	PG4	O2-C3-C4-O3
5	C	407	PG4	O2-C3-C4-O3
4	B	402	NAG	O5-C5-C6-O6
5	E	403	PG4	O3-C5-C6-O4
5	E	403	PG4	O1-C1-C2-O2
5	E	403	PG4	O4-C7-C8-O5
5	B	403	PG4	O1-C1-C2-O2
5	B	403	PG4	O4-C7-C8-O5
5	B	403	PG4	O2-C3-C4-O3
5	B	403	PG4	C1-C2-O2-C3
5	B	403	PG4	C3-C4-O3-C5

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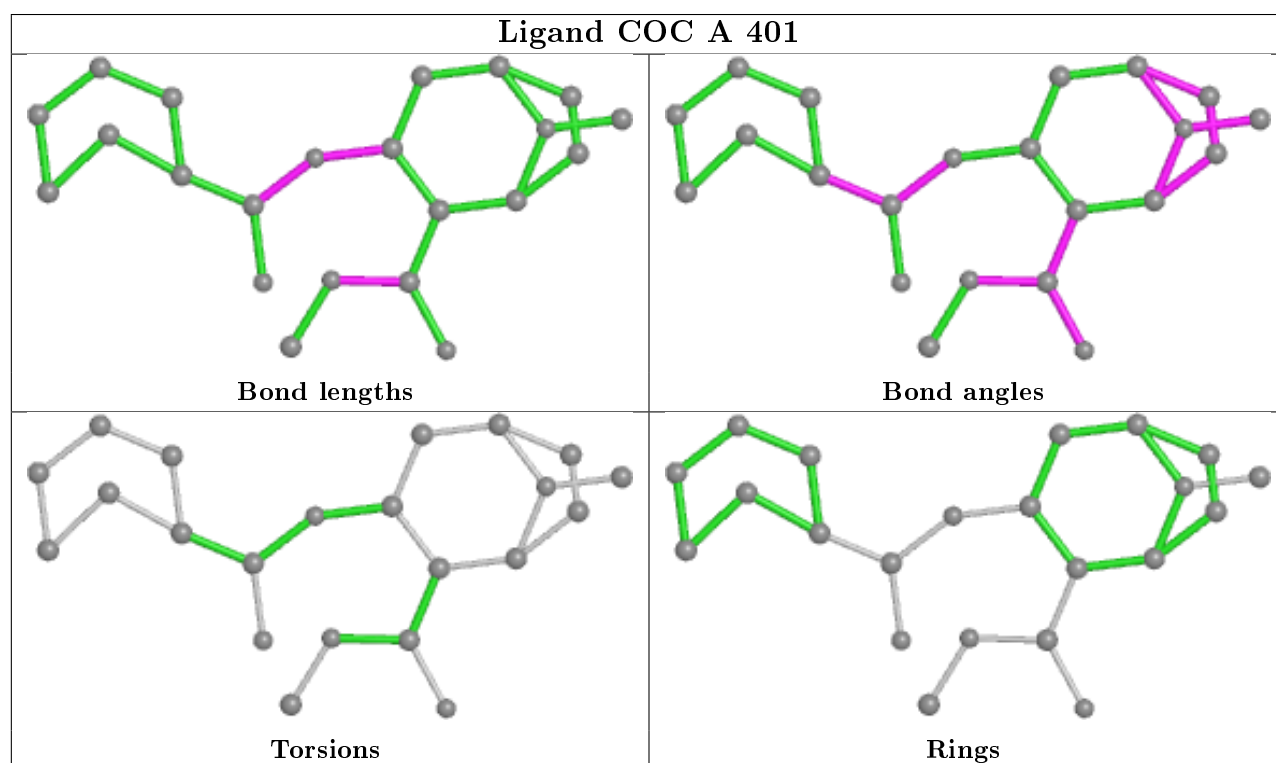
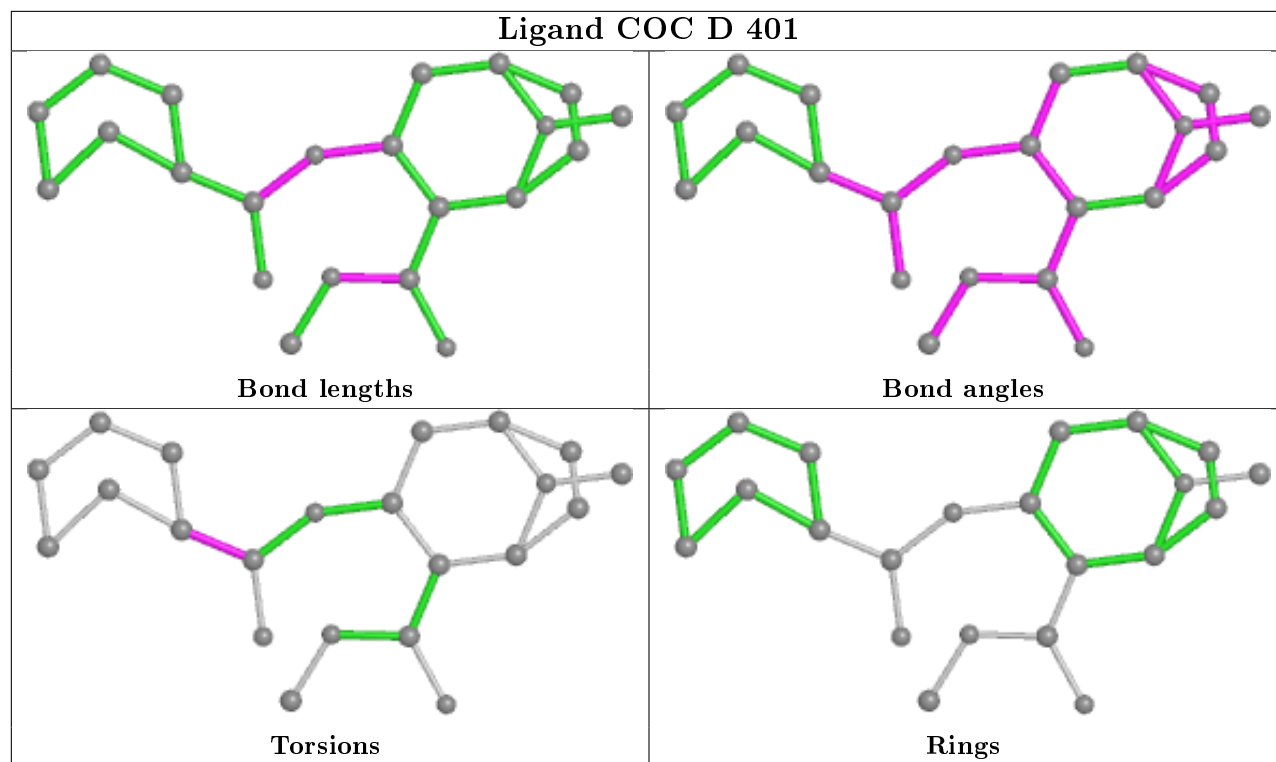
Mol	Chain	Res	Type	Atoms
5	E	403	PG4	C1-C2-O2-C3
5	B	403	PG4	C6-C5-O3-C4
5	C	407	PG4	O3-C5-C6-O4
5	B	403	PG4	C8-C7-O4-C6
5	E	403	PG4	C8-C7-O4-C6
5	E	403	PG4	C6-C5-O3-C4
5	E	403	PG4	C3-C4-O3-C5
3	D	401	COC	O1-C2-C4-C5

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	403	PG4	2	0
3	A	401	COC	1	0
5	B	403	PG4	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

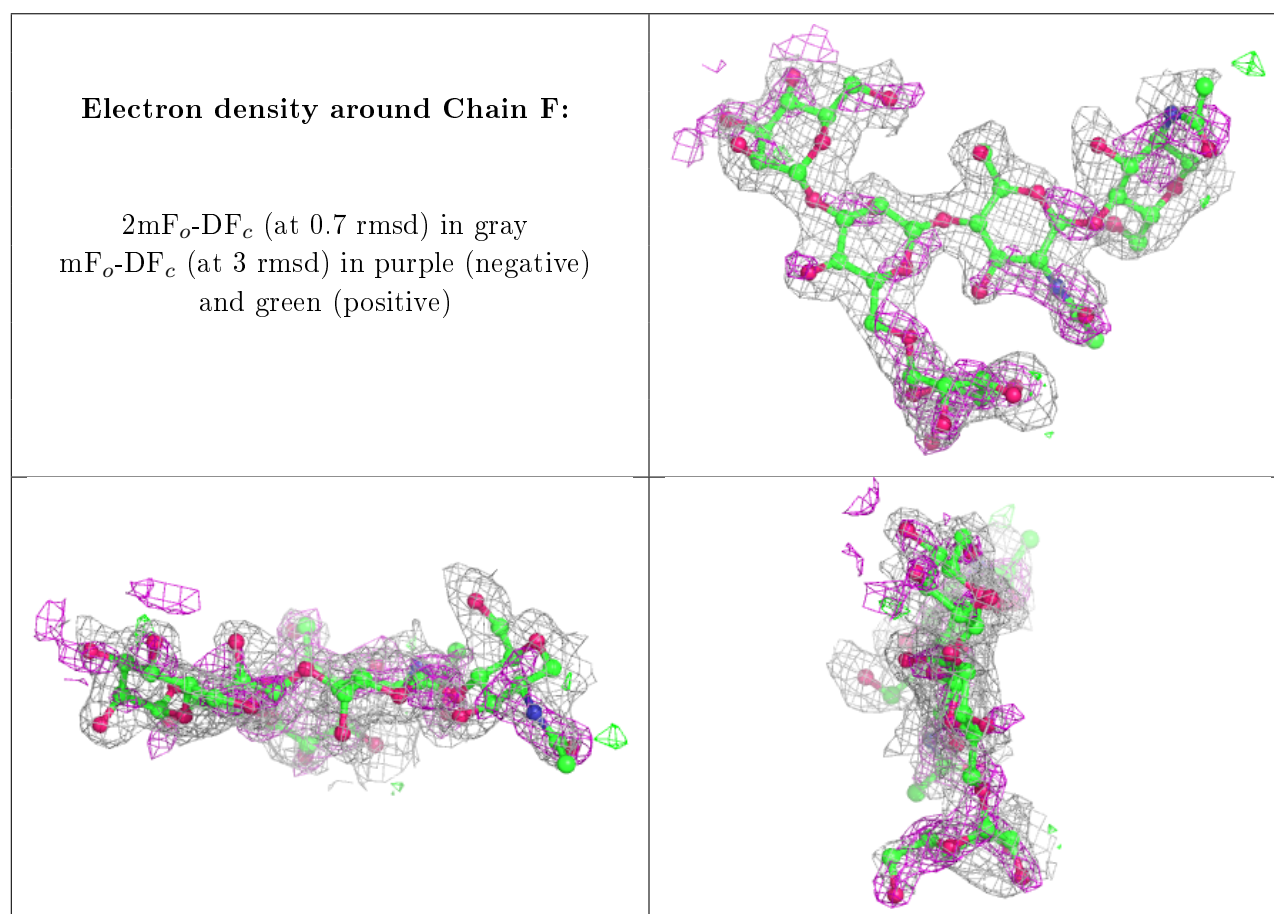
### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

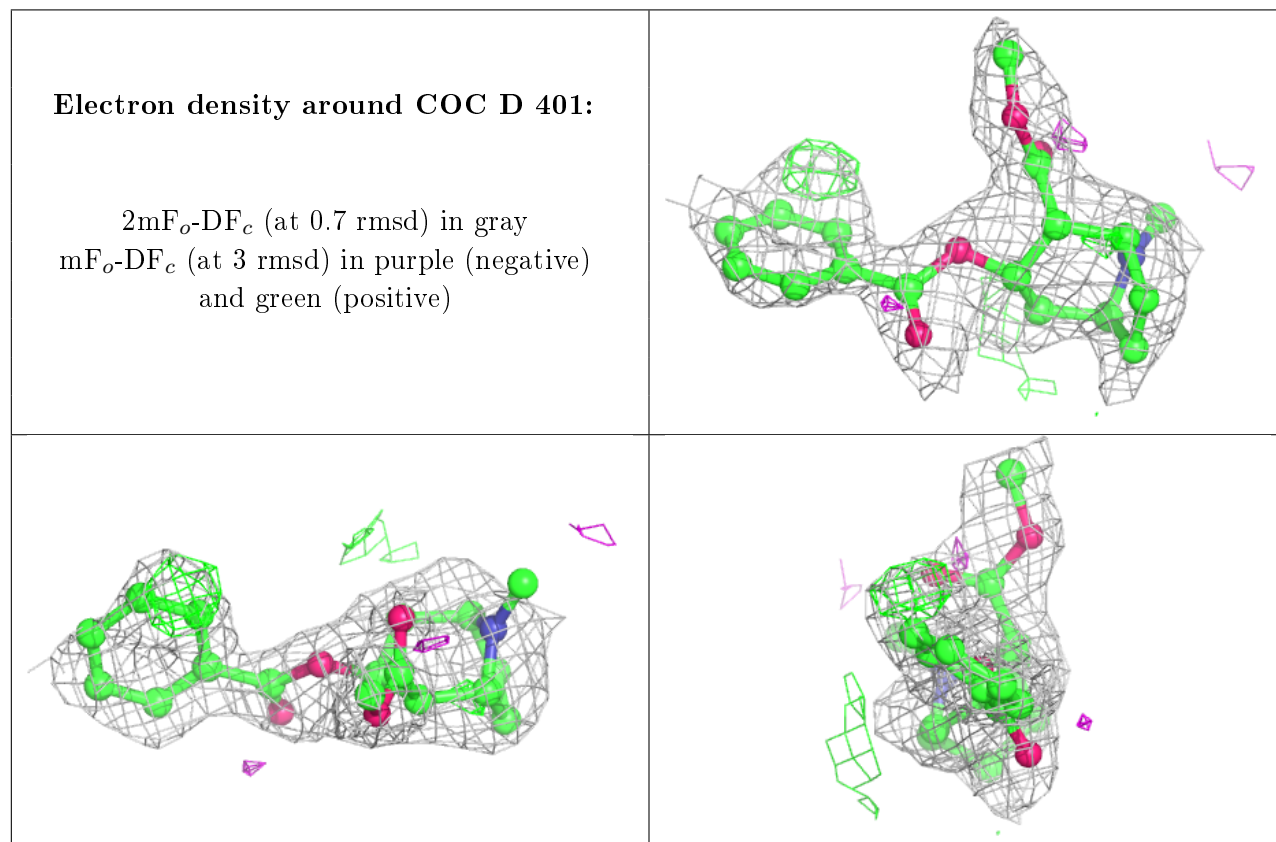


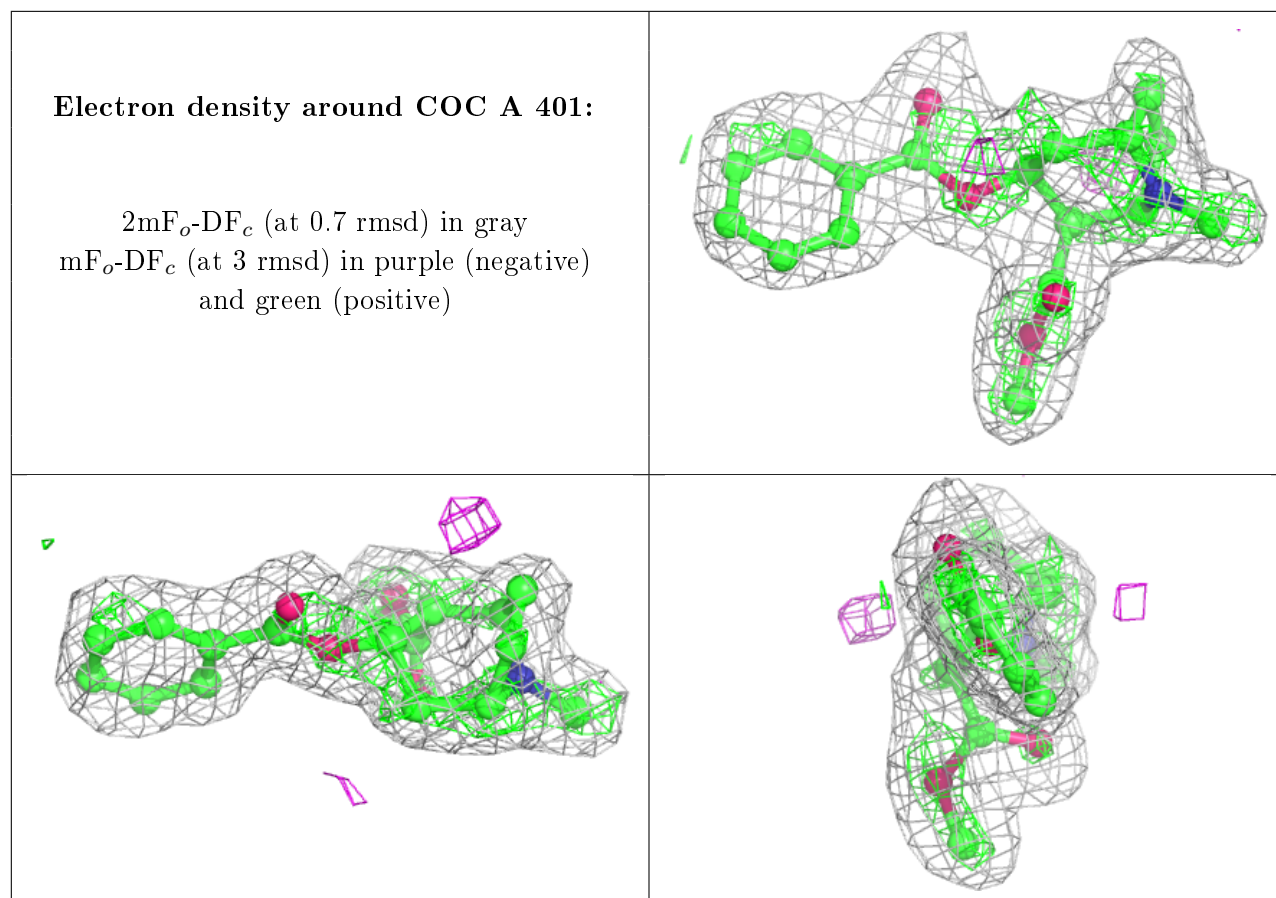
### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.



The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.